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97.8
1242
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1270
1 MSKGEELFTAVVPILVELDG......VLLEFVTAAGITHGMDELYK 238
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| Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/PCT_RM* PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/PCT_RM* PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
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6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US60_PUBGOMB.pep:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1424015 seqs, 332791073 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Result		Ouery	* Ouery			
No.	Score	Match	Length	DB	ID	Description
-	1270	100.0	!	10	US-09-575-847-2	Sequence 2, Appli
7	1270	100.0		14	US-10-071-976-2	Sequence 2, Appli
٣	1270	100.0		15	US-10-620-099-2	Sequence 2, Appli
4	1270	100.0	238	17	US-10-924-232-2	Sequence 2, Appli
S	1246	98.1		σ	US-09-884-681-2	Sequence 2, Appli
9	1246	98.1		10	US-09-967-301-2	Sequence 2, Appli
7	1246	98.1		13	US-10-024-686-2	Sequence 2, Appli
œ	1246	98.1		13	US-10-057-505-2	Sequence 2, Appli
0	1246	98.1		14	US-10-293-580-2	Sequence 2, Appli
10	1246	98.1		. 14	US-10-293-580-74	Sequence 74, Appl
11	1246	98.1		15	US-10-457-982-2	Sequence 2, Appli
12	1246	98.1		16	US-10-724-178-2	Sequence 2, Appli
13	1246	98.1		16	118-10-757-624-2	Semience 2 Appli

9

61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIIFFKDDGNYKTRAEVKFEGDTLV 120

1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL 60

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1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL

Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 159, Appli Sequence 159, Appli Sequence 159, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 6, Appli Sequence 96, Appli Sequence 96, Appli Sequence 96, Appli Sequence 100, Appli Sequence 100	IFORNIA FLUORESCENT PROTEINS	Indels 0; Gaps 0;
14 1242 97.8 238 9 US-09-920-922-4 15 1242 97.8 238 10 US-09-960-45A-125 16 1242 97.8 238 10 US-09-960-45A-125 19 1242 97.8 238 10 US-09-865-538-2 19 1242 97.8 238 10 US-09-865-511-2 21 1242 97.8 238 14 US-10-121-258-10 22 1242 97.8 238 14 US-10-136-765-10 23 1242 97.8 238 14 US-10-216-765-15 24 1242 97.8 238 14 US-10-305-765-15 25 1242 97.8 238 14 US-10-305-765-15 26 1242 97.8 238 14 US-10-305-765-15 27 1242 97.8 238 15 US-10-305-765-15 28 1242 97.8 238 15 US-10-305-765-16	ALIGNMENTS 1 575-847-2 ence 2, Application US/09575847 faction No. US20030013149A1 ALICANT: THE REGENTS OF THE UNIVERSITY OF CALLICANT: REMINGTON, James LICANT: REGENTS OF THE UNIVERSITY OF CALLICANT: REMINGTON, James LICANT: REGENTS OF THE UNIVERSITY OF CALLICANT: REGENTS OF THE UNIVERSITY OF CALLICANT: REGENTS OF SERVE APPLICATION UNMBER: US 08/974,737 OR FILING DATE: 1997-08-15 OR APPLICATION NUMBER: US 08/974,737 OR FILING DATE: 1997-08-15 OR APPLICATION NUMBER: US 08/911,825 OR APPLICATION NUMBER: US 08/911,825 OR APPLICATION NUMBER: US 08/706,408 OR FILING DATE: 1996-08-10 OR APPLICATION NUMBER: US 08/706,408 OR FILING DATE: 1996-08-30 OR PALLING DATE: 1996-08-30 OR APPLICATION NUMBER: US 08/706,408 OR PRILING DATE: 1996-08-30 OR APPLICATION NUMBER: US 08/706,408 OR APPL	.8e-119; s 0;

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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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                          181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                         Sequence 2. Application US/10620099;
Publication No. US20040014128A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
TITLE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
FILE REFERENCE: REGENT 250-5
CURRENT APPLICATION NUMBER: US/10/620,099
CURRENT FILING DATE: 2000-05-19
FRIOR PRIOR FILING DATE: 1997-01-19
FRIOR FILING DATE: 1997-01-19
FRIOR FILING DATE: 1997-08-15
FRIOR FILING DATE: 1997-08-15
FRIOR FILING DATE: 1996-08-30
FRIOR FILING DATE: 1996-08-30
SOFTWARE: PARCHING DATE: 1996-08-30
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Publication No. US20050079525A1
GENERAL INFORMATION:
APPLICANT: Taien et al., Roger Y. et al.
TITLE OF INVENTION: LONG WAVELENGTH MUTANI FLUORESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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1.8e-119;
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Pred. No. 1.
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MEDIUM TYPE: Flopp:
COMPUTER: IBM PC C
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Best Local Similarity 100.
Matches 238; Conservative
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; ORGANISM: Aequorea
US-10-620-099-2
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US-10-924-232-2
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US-10-620-099-2
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                                                                                                      121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                      181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                      181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TSIEN et al., ROGER Y. et al.
TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,976
FILING DATE: 05-Feb-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/056001
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 09/465,142
FILING DATE: 1999-DEC-16
APPLICATION NUMBER: 08/974,737
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10071976
Publication No. US20030036178A1
GENERAL INFORMATION:
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TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 238 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                          US-10-071-976-2
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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIIFFKDDGNYKTRAEVKFEGDILV 120
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                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,865
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307Z-069000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.1%; Score 1246; DB 9;
Best Local Similarity 97.9%; Pred. No. 4.7e-117;
Matches 233; Conservative 2; Mismatches 3;
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Pred. No. 4.7e-117;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stubbs, Simon L.
APPLICANT: Ordes, Anne E.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Pluorescent Proteins
FILE REFERENCE: PA0111
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: GB 0109858.1
PRIOR PILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-884-681-2
                         FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                          (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09967301; Publication No. US20030175859A1
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.9%;
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-09-967-301-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                               FELEFAX:
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TITLE OF INVENTION: Assays for Protein Kinases Using
Fluorescent Protein Substrates
                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/924,232
FILING DATE: 23-Aug-2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CORRESPONDENCE ADDRESS:
Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/071,976

FILING DATE: 05-Feb-2002

APPLICATION NUMBER: 09/465,142

FILING DATE: 1999-DEC-16

APPLICATION NUMBER: 08/974,737

FILING DATE: -Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRANICN NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07257/056001

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8e-119
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100.0%; Pred. No. 1.8
:ive 0; Mismatches
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-924-232-2
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 238 amino acids TYPE: amino acid
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Patent No. US200200061546A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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STATE: California
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Matches 238; Conservative
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Sequence 2, Application US/10293580; Publication No. US20030170767A1; GENERAL INFORMATION:
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Publication No. US20020164674A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LENGTH: 238
TYPE: PRT
ORGANISM: Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-293-580-2
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VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
                        61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                          NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                     181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                             1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPMPTL
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tsien, Roger Y.
Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windiws55
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/024,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1246; DB 13;
Pred. No. 4.7e-117;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07257/032002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/057,995
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/27,452
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: USS5/14692
FILING DATE: 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/337,915
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-024-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-Dec-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10024686
Publication No. US20020123113A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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97.9%;
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Best Local Similarity 97.9%;
Matches 233; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REPERENCE: AURO1270 (08366/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
PRIOR TFLING DATE: 2002-11-12
PRIOR APPLICATION. NUMBER: US/9/129,192
PRIOR FILING DATE: 1998-07-24
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121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                    181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 238;
                                                                                                                                                                                                                                                                                        Score 1246; DB 13;
Pred. No. 4.7e-117;
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Sequence 2, Application US/10724178; Publication No. US20040137528A1; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.9%;
Matches 233; Conservative
      US20030212265A1
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Aequorea victoria
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, ORGANISM: Aequorea victoria
US-10-724-178-2
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APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Fost-Translational Modifications
TITLE OF INVENTION: MUNICALION (0836/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                   VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                       Query Match 98.1%; Score 1246; DB 14; Length 238; Best Local Similarity 97.9%; Pred. No. 4.7e-117; Matches 233; Conservative 2; Mismatches 3; Indels 0
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Sequence 74, Application US/10293580; Publication No. US20030170767A1
GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.0 SEQ ID NO 2 LENGTH: 238
                                                                ; TIPE: FALL
; ORGANISM: Aequorea
US-10-293-580-2
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US-10-457-982-2
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APPLICANT: Michnick, Stephen
APPLICANT: Machick, Stephen
APPLICANT: Machie, Marnie
APPLICANT: Machie, Marnie
APPLICANT: Lamerdin, Janeridi, Marnie
TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
TITLE OF INVENTION: COMPLEMENTATION ASSAYS
FILE REFERENCE: ODDY007
CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT FILING DATE: 2003-12-01
PRIOR PAPPLICATION NUMBER: US 60/461,133
PRIOR FILING DATE: 2003-04-09
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GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Llopis, Juan
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: PLUORESCENT THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
PRIOR PILING DATE: 2003-06-09
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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98.1%; Score 1246; DB 16;
Best Local Similarity 97.9%; Pred. No. 4.7e-117;
Matches 233; Conservative 2; Mismatches 3;
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Pred. No. 4.7e-117;
2; Mismatches 3;
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Indels

Length 238;

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61 VITFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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Patent No. US20020099170A1

GENERAL INFORMATION:
APPLICANT: TSUKAmoto, Tobhiro
APPLICANT: TSUKAmoto, No. US20020099170A1iyo
TITLE OF INVENTION: GREEN FLUORESCENT PROTEINS AND BLUE FLUORESCENT
TITLE OF INVENTION: GREEN FLUORESCENT PROTEINS AND BLUE FLUORESCENT
TITLE OF INVENTION: QREEN FLUORESCENT PROTEINS AND BLUE FLUORESCENT
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/612,539
PRIOR APPLICATION NUMBER: US 09/121,539
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 14
SSOFTWARE: PATENTIN VET. 2.0
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97.5%; Pred. No. 1.2e-116;
tive 3; Mismatches 3;
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Pred. No. 1.2e-116;
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PRIOR APPLICATION NUMBER: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                      97.8%;
97.5%;
                                                                                                                                                                     LENGTH: 238
TYPE: PRT
ORGANISM: Aequorea victoria
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Matches 232; Conserv
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LENGTH: 238
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                       MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL
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Pred. No. 4.7e-117;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stubbs, Simon L. J.
APPLICANT: Stubbs, Simon L. J.
APPLICANT: Jones, Anne E.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FILE REFERENCE: PAOLII
CURRENT FILING DATE: 2004-01-14
PRIOR PLING DATE: 2004-09-28
PRIOR PLING DATE: 2001-09-28
STORING PLING DATE: 2001-09-28
STORING PLING DATE: 2001-09-28
SOUTWARE: PACENTING DATE: 201-09-28
SOUTWARE: PACENTIN VERSION 3.2
SOUTWARE: PACENTIN VERSION 3.2
SEQ ID NO.
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Patent No. US2002008348BA1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-01201
CURRENT APPLICATION NUMBER: US/09/920,922
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Publication No. US20040138420A1
GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 233; Conservative ;
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US-10-757-624-2
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Search completed: April 25, 2005, 15:59:51 Job time : 138 secs

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61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIIFFKDDGNYKTRAEVKFBGDTLV 120
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Sequence 159, App
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413.174 Million cell updates/sec
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/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-214-909-2
US-09-479-645A-10
US-09-479-645A-159
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US-08-679-865-2

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US-08-792-553-2

US-09-102-553-2

US-09-102-553-2

US-09-102-103-2

US-09-102-103-2

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US-09-103-103-2

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US-09-603-2

US-09-603-2

US-08-594-576-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Fatent No. 6054321
GENERAL INFORMATION:
TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,825
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/056001
TELEPHONIS: 619/678-5099
TELEPHONIS: 619/678-5099
                        US-09-023-946B-2
US-09-646-53B-2
US-09-503-222-2
US-09-472-065A-2
US-09-479-645A-96
US-09-479-645A-100
US-09-479-645A-100
US-09-479-645A-110
US-09-479-645A-110
US-09-479-645A-110
US-09-479-645A-110
US-09-127-2
US-09-127-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY:
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                                     NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                         121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                 181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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E: Fish & Richardson P.C. ,
4225 Executive Square, Suite 1400
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Pred. No. 3.
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SOCTWARE: Petentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NWBER: 08/911,825
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               Sequence 2, Application US/08974737
Patent No. 6077707
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IBM PC compatible
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07;
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100.0%;
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INFORMATION FOR SEQ ID NO: 2:
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amino acid
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238; Conservative
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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ZIP: 92037
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STATE:
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61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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Patent No. 6403374
GENERAL INFORMATION:
APPLICANT: Taien et al., Roger V. et al.
TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
                                         GENERAL INFORMATION:
APPLICANT: Tsien et al., Roger Y.
TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1270; DB 3; 100.0%; Pred. No. 3.1e-130;
                                                                                                                                                       SSEE: Fish & Richardson P.C.
I: 4225 Executive Square, Suite 1400
La Jolla
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,050
FILING DATE: 16-AUG-1996
ATTOCNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
; Sequence 2, Application US/08706408; Patent No. 6124128
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 238; Conservative
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STREET: 42
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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,976
FILING DATE: 05-Feb-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,142
FILING DATE: 1999-DEC-16
APPLICATION NUMBER: 08/974,737
FILING DATE: cUnknown>
ATTORNEY/AGRYI CUNKNOWN>
ATTORNEY/AGRYI CUNKNOWN>
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TITLE OF INVENTION: LONG WAVELENGTH MUTANT FLUORESCENT
                                                                                                                                                                                                                                                                                        Indels
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ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                       ; Score 1270; DB 4;
; Pred. No. 3.1e-130;
0; Mismatches 0;
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/056001
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TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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Patent No. 6780975
GENERAL INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
PRIOR APPLICATION NUMBER: US 08/7
PRIOR FILING DATE: 1996-08-30
NUMBER 08 SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 238
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Best Local Similarity 100.
Matches 238; Conservative
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; ORGANISM: Aequorea
US-09-575-847-2
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Fatent No. 6593135
GENERAL INFORMATION:
APPLICANT: WAGTER, Rebekka
APPLICANT: WAGTER, Rebekka
APPLICANT: REMINGTON, James
TITLE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
TILE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
CURRENT APPLICATION NUMBER: US/09/575,847
CURRENT FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 08/974,737
PRIOR APPLICATION NUMBER: US 08/911,825
PRIOR FILING DATE: 1997-08-15
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                                                                                                                                                                          COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BY POLICATION DATA: CIRROTT APPLICATION DATA: CIRROTT APPLICATION NUMBER: US/09/465 11.0
                     NUMBER OF SEQUENCES: 4
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,737
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/0!
TELECOMMUNICATION INFORMATION:
TELECHONE: 619/678-5070
TELEFAX: 619/678-5070
    PROTEINS
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amino acid
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Best Local Similarity 100.
Matches 238; Conservative
                                                                                                                                                         COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                            STREET: 42;
CITY: La Jo
STATE: CA
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENY INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFRENCE/DOCKET NUMBER: 0230
TELEPHONE: (415) 576-0200
INFORMATION: (415) 576-0200
INFORMATION: (415) 576-0300
INFORMATION: CR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 238 amino acids
amino acid
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Matches 233; Conservative
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                                                                                       Length 238;
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98.1%; Score 1246; DB 1; Length 238;
Best Local Similarity 97.9%; Pred. No. 1.3e-127;
Matches 233; Conservative 2; Mismatches 3; Indels 0
                                                                                                                                   Indels
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APPLICANT: Teien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Fluorescent Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Telen, ROGER Y.
APPLICANT: Helm, ROGER
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
FILE REFERENCE: 07257/032003
CURRENT APPLICATION NUMBER: US/08/753,143A
CURRENT FILING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                       100.0%; Score 1270; DB 4; 100.0%; Pred. No. 3.1e-130;
                                                                                                                                   0; Mismatches
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-071-976-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-679-865-2
; Sequence 2, Application US/08679865
; Patent No. 5912137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-753-143-2
                                                                                  Query Match
Best Local Similarity 100.
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 238
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61 VTTFSYGVQCFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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Sequence 2, Application US/08680876

Sequence 2, Application US/08680876

GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
TITLE OF INVENTION: Rasays for Protein Kinases Using
TITLE OF INVENTION: Fluorescent Protein Substrates
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION TO PATE: US/08/679,865
FILING DATE: 16-JUL-1996
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%; Score 1246; DB 2; 97.9%; Pred. No. 1.3e-127; iive 2; Mismatches 3;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
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Gaps

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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
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US-08-753-144-2
; Sequence 2, Application US/08753144
; Patent No. 6066476
; GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger
TTTLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTY: USA
                                                                                                                                                                                                     Length 238;
                                                                                                                                                                                                Score 1246; DB 2;
Pred. No. 1.3e-127;
2; Mismatches 3;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPRATING SYSTEM: Windiws95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/753,144
FILING DATE: 20-NOV-1996
RICH APPLICATION UNBER: US/08/753,144
APPLICATION NUMBER: US/08/753,144
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US95/14692
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APPLICATION NUMBER: 08/337,915
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                  98.1%;
97.9%;
                  information for SEQ ID NO: 2: SEQUENCE CHRARACTERISTICS: LENGTH: 238 amino acids i TYPE: amino acid TYPE: amino acid i TYPE: protein US-08-792-553-2
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Best Local Similarity 97.9
Matches 233; Conservative
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INFORMATION FOR SEQ ID NO
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TOPOLOGY:
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Patent No. 5981200
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heim, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
NUMBER OF SEQUENCES: 25
CORRESONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
RELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 619-678-5070
      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.3e
2; Mismatches
                                                                                                                                                                                              02307Z-069200
                                              FILING DATE: 16-JUL-1996
CLASSIFICATION: 435
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                LENGTH: 238 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.1
Best Local Similarity 97.9
Matches 233; Conservative
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MOLECULE TYPE: protein
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CITY: La Jolla
STATE: California
COUNTRY: USA
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US-08-680-876-2
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APPLICANT: Llopis, Juan
APPLICANT: Wachter, Rebekka M.
Miyawaki, Atsushi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-263-975-2
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                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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                                                                         Query Match 98.1%; Score 1246; DB 3; Length 238; Best Local Similarity 97.9%; Pred. No. 1.3e-127; Matches 233; Conservative 2; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SENSORS FOR IE PH OF A BIOLOGICAL SAMPLE
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Pred. No. 1.3e-127;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09094359
Fatent No. 6140132
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Hispan, Atlanshi
APPLICANT: Miyawaki, Atlanshi
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSC
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSC
FILE REFERENCE: 07257/067001
CURRENT APPLICATION NUMBER: US/09/094,359
CURRENT FILING DATE: 1998-06-09
CURRENT FILING DATE: 1998-06-09
CURRENT FILING DATE: ADMOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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ilarity 97.9%;
Conservative 2
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US-09-094-359-2
 protein
internal
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Best Local Similarity
Matches 233; Conserv
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-753-144-2
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US-09-172-063-2
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; Sequence 2, Application US/09172063; Patent No. 615017 GENERAL INFORMATION: APPLICANT: Tsien, Roger Y.

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61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEELFTAVVPILVELDGDVNGHKRSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
APPLICANT: Reminder, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09263975

Sequence 2, Application US/09263975

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tablen, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using TITLE OF INVENTION: Pluorescent Protein Substrates NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,975
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1246; DB 3;
Pred. No. 1.3e-127;
2; Mismatches 3;
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REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 023072-069000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/679,865
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.1%;
Best Local Similarity 97.9%;
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Aequorea victoria
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61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLAD 180
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APPLICANT: Telen, Roger
TITLE OF INVENTIONS FLUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
FILE REFERENCE: 07257/03201
CURRENT FILING DATE: 1996-03-20
EARLIER APPLICATION NUMBER: US/08/727,452A
EARLIER APPLICATION NUMBER: DCT/US95/14692
EARLIER PILING DATE: 1995-11-13
EARLIER PILING DATE: 1994-11-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                              Score 1246; DB 3; Length 238;
Pred. No. 1.3e-127;
2; Mismatches 3; Indels
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Pred. No. 1.3e-127;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-727-452-2
; Sequence 2, Application US/08727452A
Patent No. 6319669
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                   TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0200 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.9%;
Matches 233; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.1%;
Best Local Similarity 97.9%;
Matches 233; Conservative
                                                                                                   LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-263-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-727-452-2
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LENGTH: 238
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Db 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
Search completed: April 25, 2005, 15:48:17
Job time: 45 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 25, 2005, 15:36:47; Search time 40 Seconds Run on:

(without alignments) 572.490 Million cell updates/sec

US-10-620-099-2 1270 1 MSKGBELFTAVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	-
Result No.	Score	Query	Length	DB	ΩI	Description
н	1236	97.3	238	-	JQ1514	green-fluorescent
7	105.5	8.3	785	~	H72228	hypothetical prote
ო	100.5	7.9	887	~	E82590	
4	66	7.8	336	7	C64468	hypothetical prote
2	.92.5	7.3	2573	7	D71614	
9	90	7.1	471	7	T27856	3]
7	90	7.1	797	7	JC4078	protective surface
œ	06	7.1	808	N	F64102	protective surface
σ	89.5	7.0	393	0	C64613	conserved hypothet
10	88.5	7.0	312	7	C81710	thioredoxin reduct
11	88.5	7.0	425	0	C97354	hypothetical prote
12	87.5	6.9	861	~	H64102	
13	87	6.9	822	7	C71633	ATP-dependent nucl
14	87	6.9	2334	N	S32920	cell wall-associat
15	98	6.8	357	~	G81355	tRNA (uracil-5-)-m
16	85.5	6.7	752	7	KXRTC1	proprotein convert
17	85.5	6.7	836	٦	JDVLD	DNA-directed DNA p
18	85.5	6.7	889	~	JC5576	inter-alpha-trypsi
19	84.5	6.7	351	7	B71556	probable thioredox
20	84.5	6.7	860	~	AC0582	leucyl-tRNA synthe
21	83	6.5	281	7	AD2052	hypothetical prote
22	83	6.5	533	~	S47271	AHNAK-related prot
23	83	6.5	1092	~	S42798	fibronectin-bindin
24	83	6.5	3472	~	T31308	hypothetical 367K
25	82.5	6.5	613	7	A99552	oligoendopeptidase
56	82.5	6.5	1134	~	A60234	IgA Fc receptor pr
27	82.5	6.5	1164	Н	FCSOAG	Fc receptor
28	82	6.5	207	~	C70483	
29	82	6.5	653	н	AI1535	fructose-bisphosph

pothetical prote	pothetical prote	A polymerase III	pothetical prote	pothetical prote	obable membrane	oteoglycan link	iquinol-cytochro	pothetical prote	A topoisomerase	hypothetical prote	pothetical prote	A-directed DNA p	bacitracin synthet	incharacterized pr	hypothetical prote
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T25	T41	. B83	G20	. H89	855	LKC	823	C20	D83	ABI	G71	. A36	T31	C97	E82
764 2	1082 2	1433 2	2166 2	647	953	355 1	504	636	655 2	1334 2	1346 2	2222	6359 2	311 2	393 2
6.5	6.5	6.5	6.5	6.4	6.4	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3
82	82	82	82	81	81	80.5	80.5	80.5	80.5	80.5	80.5	80.5	80.5	80	80
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	
JQ1514	
green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)	
C;Species: Aequorea victoria	
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 09-Jul-2004	
C, Accession: JS0692, JQ1514, PQ0335; S48693; S51330; S51331	
R; Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.	
Gene 111, 229-233, 1992	
A, Title: Primary structure of the Aequorea victoria green-fluorescent protein.	
A; Reference number: JQ1514; MUID: 92175527; PMID: 1347277	
A;Accession: JS0692	
A; Molecule type: DNA	
A;Residues: 1-107,'S',109-238 <pra1></pra1>	
A, Cross-references: UNIPROT: P42212; UNIPROT: Q17106; UNIPROT: Q17105; GB: M62654; NID: 915:	IID:915:
A;Accession: JQ1514	1
A;Molecule type: mRNA	
A;Residues: 1-99,'F',101-140,'L',142-218,'V',220-238 <pra2></pra2>	
A; Cross-references: GB: M62653; NID: 9155660; PIDN: AAA27721.1; PID: 9155661	
A;Accession: P00335	
A;Molecule type: protein	
A; Residues: 46-64; 74-122; 132-151; 154-183; 185-200 < PRA3>	
R;Inouye, S.; Isuji, F.I.	
FBBS Lett. 351, 211-214, 1994	
1.Title: Ruidence for redox forms of the Aemiores green fluorescent protein	

A;Title: Evidence for redox forms of the Aequorea green fluorescent protein.

A;Accession: S48693; MUID:94364470; PMID:8082767

A;Accession: S48693

A;Status: preliminary

A;Accession: S48693

A;Status: preliminary

A;Accession: S48693

A;Status: preliminary

A;Accession: Campbell, A.K.

B;Matkins, J.N.; Campbell, A.K.

S;Matkins, J.N.; Campbell, A.K.

S;Matkins, J.N.; Campbell, A.K.

S;Matkins, J.N.; Campbell, A.K.

S;Matkins, J.N.; Campbell, A.K.

A;Accession: S51330

A;Accession: S51330

A;Accession: S51330

A;Accession: S51330

A;Accession: S51330

A;Experimental source: clone gfpl

A;Experimental source: clone gfpl

A;Experimental source: clone gfpl

A;Accession: S5133

A;Molecule type: mRNA

A;Residues: 1-24, Q', Z6-29, R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q'

A;Cross-references: EMBL:X83950; NID:9634010; PIDN:CAA58790:1; PID:9634011

A;Accession: S5133

A;Molecule type: mRNA

A;Residues: 1-24, Q', Z6-29, R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q'

A;Cross-references: EMBL:X83950; NID:9634010; PIDN:CAA58790:1; PID:9634011

A;Accoss-references: EMBL:X83950; NID:9634010; PIDN:CAA58790:1; PID:9634011

A;Accoss-references: EMBL:X83950; NID:9634010; PIDN:CAA58790:1; PID:9634011

A;Reference number: A65692; PDB:1GFL

A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-A;Contents: annotation; X-ray cryteallography, 1.9 angstroms, Residues 'A', 2-79, 'R', 81-A;Contents: annotation; Y-ray cryteallography, 1.9 angstroms, Residues 'A', 2-79, 'R', 81-A;Contents: annotation; Y-ray cr

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Matches 4
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.Contents: annotation; X-ray crystallography, 1.9 angstroms (see PIR:AQJFNV) emittin ;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin ;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hickey
on, D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
Ajritle: Evidence for lateral gene transfer between Archaea and Bacteria from genome Ajritle: Evidence for lateral gene transfer by PMD:10360571
Ajrecession: H72228
Ajrecession: H72228
Ajrecession: Lype: DNA
Ajrecelle type: DNA
Ajrecile type: DNA
Ajreciles: 1-785 <ARN>
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITESYGVOCFSRYPDHMKRHDFFKSAMPEGYVQORIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFYKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NRIELKGIDFKEDGNILGHKMEYNYNSHNVYIMADKQKNCIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 RYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DVNGH------KFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NEDLFKEIEDREWIYERBFFKEDVKEGERVDLVFEGVDTLSDVYLNGVYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADYYQQNTPILDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTXGKLTLKFICTTGKLPVPWPTL
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| DLNGFWSVRDNEGRFSFEGTVPG-VVQADLVRK-----GLLPHPYVGM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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                       A;Contents: annotation; X-ray crystallography, 1.9 angstroms C;Comment: This protein is excited by the photoprotein aequorin (se C;Comment: The chromophore of this protein is formed by modification C;Goment: The chromophore of this protein is formed by modification C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Superfamily: green-fluorescent protein
C;Superfamily: 5-imidazolinone (Ser-Gly) #status experimental
F;65/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 785;
                                                                                                                                                                                                                                                                                                                                      Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                Query Match 97.3%; Score 1236; DB 1;
Best Local Similarity 96.2%; Pred. No. 1.2e-95;
Matches 229; Conservative 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; Score 105.5; DE 23.9%; Pred. No. 0.84; iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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43; Conserv
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Best Local S
Matches 43
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leucyl-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)

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C;Species: Xylella fastidiosa
C;Date: 18-Aug.2000 #sequence_revision 20-Aug.2000 #text_change 02-Sep-2000
C;Date: 18-Aug.2000 #sequence_revision 20-Aug.2000 #text_change 02-Sep-2000
R;Accession: E82590
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; MID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1887 cSIM>
A;Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN00
A;Experimental source: strain 95.cc
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreitra, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.B.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
C.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
C.A.; Martins, E.M.F.; Matsukuma, A.Y.; Mario, C.I.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; March, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Roditjues, V; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.;
A;Reference number: A59328
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C;Genetics:
A;Map position: FOR1295121-1296131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RQGRGQRRVNYRLR----DWGVSRQRYWGCPIPVIYCPTCGAVPVPEDQLPVILPEN 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :| | : | | : | | : | TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 TTGKLLPVPWPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: XF2176
C,Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAFSGTGSPIKTDPEWRK
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C;Accession: JC4078
R;Flack, F.S.; Loosmore, S.; Chong, P.; Thomas, W.R.
Gene 156, 97-99, 1995
A;Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus inf
A;Reference number: JC4078; MUID:95255676; PMID:7737523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: JC4078
A; Molecule type: DNA
A; Molecule type: DNA
A; Rossides: 1-797 cFLA>
A; Cross-references: UNIPROT: P46024, GB:U13961, NID:g537447; PIDN:AAA85645.1; PID:g53744
A; Experimental source: type b
A; Experimental source: type b
C; Superfamily: protective surface antigen D-15
C; Superfamily: protective surface antigen
F; 1-19/Domain: signal sequence #status predicted <SIG>
                          A;Accession: T27856
A;Accession: T27856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-471 <FUL>
A;Residues: 1-471 <FUL>
A;Coss-references: UNIPROT:Q23488; EMBL:U00047; PIDN:AAA50686.1; CESP:ZK418.2
A;Experimental source: strain Bristol N2
C;Genetics:
C;Genetics:
A;Experimental source: 139/1; 139/1; 241/2; 295/3; 329/3; 381/3; 454/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK418.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 VPNSYKILDKIFTGEKVPQCDWVFTVKDGSP--SDFHVHGPVLADSSIVMRAAVVSHMSI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 DHMKRHDF-------PKSAMPEGYVQQ------RTIFFKDDGNYKTRA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 ASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNVFFENYDNSKSDT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 NGIKVN-FKIRHNIEDGSVQLADYYQQNTPI-LDGPVLLP--DNHYLSTQSALSKDPNEK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 NGIKTNDFDFSFGWNYNSLNRGYFPTKGVKASLGGRVTIPGSDNKYYKLSADVQGFYPLD 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VNGHK-----FSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFSRYP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Variety: type b
C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 FF---KDD-GNYKTRAEVKFE-----GDTLVNRIELKGIDFKEDGNILGHKLEYNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 FICTTGKLPVPWPTLVTTFSYGVQCFSRYPDHMKRHDF---FKSAMPE----GYVQQRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 SHNVYIMADKQKNGIKV-NFKIRHNIEDGSVQLADYYQQNTPILDGPVLL-----
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F;20-797/Product: protective surface antigen D-15 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protective surface antigen D-15 precursor - Haemophilus influenzae (type C,Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
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                                                                                                                                                                                                                                                                                                                                     DB 2; Length 471;
                                                                                                                                                                                                                                                                                                                               ch 7.1%; Score 90; DB 2; Length 471
1 Similarity 23.3%; Pred. No. 8.5;
49; Conservative 34; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 EVKFEGDTLVNRIELKGIDFKEDGNI---LGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 -PDNHYLSTQSALSKDPNEKRDHMVLLEFV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| :| |: : | 334
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  A; Reference number: Z20430
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 49
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Best Local S:
Matches 52
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R;Gardner, M.J.; Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.;
F; Percea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: D71614
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Residues: 1-2573 <GAR>
;Cross-references: UNIPROT:096185; GB:AE001396; GB:AE001362; NID:93845188; PIDN:AAC7188
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                              -----PTLVTTFSY--GVQCFSRYPDHMKR-------HDFFKSAMPEGYVQQRTIF
                                                                                                                 Gaps
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                                                                                                                                                                  ----GEGDVTYGKLTLKFICTTGKLPVPW----
                                                                                                           65; Indels 104;
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                                                    Score 99; DB 2; Length 336;
Pred. No. 0.97;
); Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGPVLLPDNHYLSTQSALSKD-PNEKRDHMVLLEFV 224
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Best Local Similarity 26.2%; Pred. No. 48;
Matches 34; Conservative 31; Mismatches
                                                                                                           40;
                                                                                                                                                               19 DGDVNGHKFSVSGE-----
                                                       1 7.8%;
Similarity 24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone 3D7
                                                                                                              Conservative
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A; Residues: 1-2573 <
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A;Start codon: TTG
                                                                                                              67;
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                                                    Query Match
Best Local S
Matches 67
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thioredoxin reductase frameshift TC0375 [imported] - Chlamydia muridarum (strain Nigg) C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C; Accession: C81710 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res. 28, 1397-1406, 2000
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97354
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
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A;Experimental source: strain Nigg (MoPn)
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A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: CB1710
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <TET>
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                                                                                                    34 EGDVTYGKLTLK------FICTTGKLPVPWPTLVTTFSYGVQCFSRYPDHMKRH--
Gaps
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A,Gene: TCO375
C,Superfamily: thioredoxin reductase, thioredoxin reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
75;
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                                                                                                                                                                                                                     174 QGD---GRLVLESMPNHRCEKIFV----HFPVPW
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Mismatches
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42;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 SQKGI 392
51;
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                                                                                                                                                                                                                                                                                                                                                                                                                         protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus Hamb, R.D.; Requencing A.D.; Rither, B.D.; Retaley, J.M.; Weldman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley,
Cience 269, 496-512; 1995
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: L-808 4TIGR.
A;Cross-references: GB:L42023; TIGR:H10917
C;Superfamily: protective surface antigen D-15
C;Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein HP0747 - Helicobacter pylori (strain 26695)
C.Species: Helicobacter pylori
C.Accession: C64613
R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A.Althors Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A. Althors Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A. Picference number: A64520; MUD: 97394467; PMID: 9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: C64613
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Residues: 1-393 <TOM>
A;Cross-references: UNIPROT:O25443; GB:AE000587; GB:AE000511; NID:g2313869; PIDN:AAD0779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 EVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNSHNVYIMADKQK- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IGYGTESGISYQ 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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Pred. No. 7.3;
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                                                                                                                            | | | | : : : | | : | RDHLWVVSAKASAGYANG 632
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Best Local Similarity
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A;Cross-references: UNIPROT:09ZCJ7; GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA151
A;Experimental source: strain Madrid E
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C;Species: Bacillus subtilis
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S32920; E69730; T47101
R;Foster, S.J.
Mol. Microbiol. 8, 299-310, 1993
A;Title: Molecular analysis of three major wall-associated proteins of Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-dependent nuclease chain A (addA) RP734 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Datces: Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: C71633
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: C71633
A;Accession: C71633
A;Acceule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 WPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 SDRINL------KENLPILDLIAAAKFVLLPDDDL--NLACLLKSPIIGISEQKL 606
--NIEDGSVQLADYYQQNTPILDGPVLLPDNHYL-STQSAL 207
                           117 DTLVN----RIELKGI-----DPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 KIRHNIEDGSVQLADYYQQNTPILD-----GPVLLPDNHYLSTQSALSKDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 87; DB 2; Length 822;
25.2%; Pred. No. 31;
tive 28; Mismatches 54; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 ----NEXRDHMVLLEFVTAAGITHGMD----ELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 YTLLVKKNDHTLWEVLSSHKDIYHKLDSIIEIYK 640
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54; Conservative
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                                                                                                208 SKDPN 212
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  165 FKIRH---
                                                                                                                                 : |||
468 NADPN
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                                                                                                                                      A;Cross-references: UNIPROT:097CY8; GB:AE001437; PIDN:AAK81622.1; PID:g15026806; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                    A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A,Reference number: A96900, MUID:21359325, PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P43827; GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. Barndon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Fritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                            Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ITGKLPVPWPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                         58 PTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTR----AEV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 YNPTILTDGEKFDKOMYNKILKEYGDESVAYSKYY-EHTLTEDYIKTLPDGYF--TSKGL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI---KVN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 SEVVKNFKNGVGDI-----KDNFVKAVKSEDKVMGNP---SGEGNYSTEEWYNYLKE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 -NVYIMADKOKNGIKVNFKIRHNIEDGSVQLADYYQQNTPILDGPVLLPDNHYLSTQSAL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 TKQAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGVGKRQVN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternate names: leucyl-tRNA synthetase;
Species: Haemophilus influenzae;
bate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 TGDKLPI-WVANFVLMHYGTGAVMAVPAHDQRD--FEFAQKYSLPIKQVIAPLADEEIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: leuS
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 861;
                                                                                                                                                                                                                                                                                            Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-861 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFEGD-----TLVNRIELKGIDFKE--DGNILGHKLEYNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                          82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
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                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                          7.0%; Score 88.5; DE 24.3%; Pred. No. 9.9; ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guery Match
6.9%; Score 87.5; D.
Best Local Similarity 24.3%; Pred. No. 30;
Matches 45; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             GDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGK-
Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                          59; Conservative
                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <KUR>
                                                                                                                                                                                                                                                                                                                   Similarity
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C;Date: 18-Aug-1995 #
C;Accession: H64102
                                                                       A; Accession: C97354
                                                                                                                                                                                                                                            A; Gene: CAC3702
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Best Local S:
Matches 59
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A;Residues: 1-2334 «KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CABIS959.1; PID:g2636469
A;Experimental source: strain 168
R;Yoshida, K.; Sano, H.; Seki, S.; Oda, M.; Fujimura, M.; Fujita, Y.
Microbiology 141, 337-343, 1995
A;Title: Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome contain A;Reference number: Z24350; MUID:95219088; PMID:7704263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Accession: G81355
Fig. Parkhilli, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin G.; W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A.Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A.Reference number: A81250; MUID:20150912; PMID:10688204
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1054 DENGHVTSITGPKNKKVTYSYENDLLKKVTDTDG-----TVTSYDYDSEGRLVKQYS 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1106 ANSTEAKPVFTEYQYSGHRLEKAINAKKETYVYSYDADKKTLLMTQPNGRKVQYGYNEAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1286 SASTNILKDGSFEAQKSGWNLTASKDRRKISVIADKSGVLSGSKALEVLSQSTSAGTDHG 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1226 ETYEYNKANDVTKAKDTEGNVTDIAYDGLDAVSETDQSGKSSSAAVYDKYGNQIQSSKDL 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 LEYNYNSHN-VYIMADKQKN-----GIKVNFKIRHNIEDGSVQLADYY----QQNTPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-2334 <YOS>
Cross-references: EMBL:D31856; NID:g603765; PIDN:BAA06656.1; PID:g603782;
Experimental source: strain BGSC1A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                                                                                              Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA
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C,Superfamily: cell wall-associated protein wapA
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A;Molecule type: DNA
A;Residues: 1-357 <PAR>
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A;Gene: trmA; Cj0831c C;Keywords: methyltransferase; S-adenosylmethionine

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                                Gaps
                                62;
                                                                                                                            -----NRIELK--GIDFKEDGNILGHKLEYNYN
                                                                                                                                                                                                           Length 357;
                                44; Indels
                                                                                                                                                                                           147 -SHNVYIMADKOKNGIKVNFKIRH-----NIEDGSVQLADYYQQN
                                                                79 KRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKF--EGI
 DB 2;
Query Match 6.8%; Score 86; DB Best Local Similarity 21.8%; Pred. No. 13; Matches 36; Conservative 23; Mismatches
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YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter.
NCBI _TaxID=354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=DSN2289;
Koranyi P., Berenyi M., Burg K.;
Submitred (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF224969; AAN86140.1; --
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26914 MW; F84840F1F9064018 CRC64;
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Last annotation update)
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Pred. No. 6.3e-93;
2; Mismatches 3;
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InterPro; IPR011584; GFP_like.
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfan; PF01353; GFP; 1.
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Q66PV5
Q66PV1
Q66PV3
Q66PV3
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Q8MMA2
Q66ND5
Q66ND5
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97.9%;
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Name=2289Gfp;
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Best Local Similarity 97.9'
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ID GFP_AEQVI
AC P42212; Q17104; Q27903;
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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MEDLINE=97299832; PubMed=9154981; DOI=10.1023/A:1005740823703; Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.; "Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage."; Plant Mol. Biol. 33:989-999(1997).
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MEDLINE=99238303; PubMed=10220315; DOI=10.1021/bi9902182;

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25-OCT-2004 (Rel. 45, Last annotation update)
Green fluorescent protein.
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         WWW="http://www.expasy.org/spotlight/articles/spt1t011.html'
      TISSUE SPECIFICITY: Photocytes.
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2, USO662; UQL514.
3, IB9C; X-ray; A=1-238.
3, IBFP; X-ray; A=1-238.
3, ICV7; X-ray; A=1-238.
3, ICV7; X-ray; A=1-238.
3, IEMA; X-ray; G=1-238.
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Pseudomonadaceae; Azomonas.
NCBI_TaxID=116849;
                                                                                                                       Azotrobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324405; AAN86137.1; -.
HSSP; P42212; 1BFP.
                                                                                                                                                                                                                Koranyi P., Berenyi M., Burg K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF324407; AAN86139.1; -.
                                                                                                                                                                                                                                                        HSEP; TATELLY IBBC.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR011584; GFP_like.

InterPro; IPR011584; GFP_related.

InterPro; IPR010786; Green_fl_protein.

PRINTS; PR01229; GFLUORESCENT.

PRODOM; P013756; Green_fl_protein; 1.

SEQUENCE 238 AA; 26886 MW; EA5A6F21FBFB6E05 CRC64;
                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Green fluorescence protein.
                                 238 AA
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InterPro; IPR009017; GFP like.
InterPro; IPR011584; GFP_related.
InterPro; IPR00786; Green_fl_protein.
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                                                                                               Green fluorescence protein.
Name=289Gfp;
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Matches 232; Conservative
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                                                                                                                                                                  NCBI_TaxID=354;
                                                                                                                                                                                                          STRAIN=CCM289;
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Q71RY9;
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     RESULT 3
Q71RY9
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3; Indels
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Pred. No. 1.3e-92;
3; Mismatches 3;
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Matches 232;
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01-NOV-1996 (TEMBLEE). 01,
01-OCT-2003 (TEMBLEE). 25,
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Aequoreidae; Aequorea.
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                                                                                                           Q93125;
01-FEB-1997
01-FEB-1997
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Pseudomonadaceae; Azotobacter.
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Koranyi P., Berenyi M., Burg K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26887 MW; E0E1616BD2AF6188 CRC64;
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Last annotation update)
                                                                                                         Score 1241; DB 2;
Pred. No. 1.6e-92;
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Pred. No. 1.9e-92;
                                                                                                                                                 2; Mismatches
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                                                                                                       Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative
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Best Local Similarity
Matches 232; Conserv
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61 VŢŢFGYĠVQCFARYPDHMKQHDFFKSAMPEGYVQERŢĪFFKDDGNYKŢRAEVKFEGDŢLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDILINE=96505137; PubMed=8707053; DOI=10.1016/0378-1119(95)00685-0; Cormack B.P., Valdivia R.H., Falkow S.; FACS-optimized mutants of the green fluorescent protein (GFP)."; Gene 173:33-38(1996).
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Yeast-enhanced green fluorescent protein (yEGFP) a reporter of expression in Candida albicans.";
Microbiology 143:303-311(1997).

EMBL; U73901; AAB18957.1; -
PDB; 2YFP; X-ray; A=1-238.

GO; GO:0006091; P:energy pathways; IEA.
InterPro; IRR001961; GFP_like.
InterPro; IRR011584; GFP_related.
InterPro; IRR001986; Green_fl_protein.
                                                                                                                                                                                                           Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97195776; PubMed=9043107;
Cormack B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,
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SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;
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ilarity 96.6%; Pred. No. 4.9e-92;
Conservative 4; Mismatches 4;
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238 AA
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                                                           Created)
                                                     01-FEB-1997 (TrEMBLrel, 02, Creat 01-FEB-1997 (TrEMBLrel, 02, Last 01-OCT-2003 (TrEMBLrel, 25, Last Green fluorescent protein mutant Manacann
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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                   181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22726112; PubMed=12693991; DOI=10.1042/BJ20021966;
Gurskaya N.G., Fradkov A.F., Pounkova N.I., Staroverov D.B.,
Bulina M.E., Yanushevich Y.G., Labas Y.A., Lukyanov S., Lukyanov K.A.;
"A colourless green fluorescent protein homologue from the non-
fluorescent hydromedusa Aequorea coerulescens and its fluorescent
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VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutants.";

Biochem. J. 373:403-408(2003).

EMBL; ANTSIDGS; AAN41637.1; -.

HSSP; P42212; BBC.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR000786; Green_fl_protein.

Pfam; PF01353; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

PRODON; PD013756; Green_fl_protein; 1.

SEQUENCE 238 AA; 26896 MW; DE72EDBB7ED9F9FE CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
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01-MAR-2002 (
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Best Local S
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Q8WP95
ID Q8WP95
AC Q8WP95;
DT 01-MAR-OT 01-MAR-OT
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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                                   the EMBL/GenBank/DDBJ databases
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238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
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238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                   Score 1200; DB 2;
Pred. No. 3.3e-89;
8; Mismatches 8;
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         Watkins J. N., Campbell A. K.;
Submitted (JAN.1995) to the EMBL/GenBank/
Submitted (JAN.1995) to the EMBL/GenBank/
EMBL; X83959; CAAS8789.1; -
PIR; J80682; JQ1514.
HSSP; P42212; IGFL.
GO GO:0006091; P:energy pathways; IEA.
InterPro; IPR00191; GFP_Inke.
InterPro; IPR01584; GFP_related.
InterPro; IPR01584; Grem_fl_protein.
Pfam; PF01353; GFP; I.
PRNTS; PR01229; GFLUCRESCENT.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sand
01-OCT-2003 (TrEMBLrel. 25, Last and
Green fluorescent protein (Fragment)
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PRINTS; PR01229; GFLUORESCENT.
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93.3%;
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Matches
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Aeguorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
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NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                       Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang Li, S.J., Xia N.S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AX013824; AAK02052.1; -.
EMBL; AX013821; AAK02059.1; -.
                                                      Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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llarity 81.1%; Pred. No. 6.4e-79;
Conservative 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.0%; Score 1079; DB 2; Length 2 ilarity 81.5%; Pred. No. 2.1e-79; Conservative 21; Mismatches 23; Indels
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan E
Li S.J., Xia N.S.;
Submitred (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF4534311, AAL33916.1;
HSSP; P42212; 1KYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AA; 27049 MW; 8185D0E5E529012B CRC64;
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238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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Pfam; PF011353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
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                                Green fluorescent protein.
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Best Local Similarity
Matches 194; Conserv
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Matches 193; Conserv
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                 61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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VTTFSYGVOCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                               NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen
Li S.J., Xia N.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aequorea macrodactyla.
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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Last sequence update)
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Last annotation update)
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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                      181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                              YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435428, AAL33913.1; -.
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80.3%; Pred. No. 5e-78;
ive 21; Mismatches 26; Indels
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Last sequence update)
Last annotation update)
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GO; GO:0006091; P:energy pathways; IEA.

Pfam; PF01135; GFP; I.

PRINTS; PR01229; GFLUORESCENT.

SEQUENCE 238 AA; 27031 MW; 5F80A19C
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Job time : 182 secs
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                                                                                                                                                                                                                                                                                                                                          Green fluorescent protein.
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Matches 191; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Name=GFP;
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Q8WTC9
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SEQUENCE FROM N.A.
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL
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Li S.J., Xia N.S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435429; AAL33914.1; --
HSSP; P42212; 1KYP.
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
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80.3%; Pred. No. 5e-78;
"Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                             26; Indels
                                                                                        Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435427; AAL33912.1; -. HSSP; P42212; IRVA
GO; GO:0006691; P:energy pathways; IEA.
PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26997 WW; SF80A192173CB84D CRC64;
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
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Last annotation update)
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; Pred. No. 4.2e-78;
21; Mismatches 26;
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80.3%; Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.5%
Matches 191; Conservative
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Chen M.

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This sequence is the wild type Aequorea victoria green fluorescent protein. The nucleic acid was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GPP) but differing by at least the substitution T203X(X=H,Y,W) or F) and having fluorescent properties different from GPP. (II) are useful as reporter molecules in immunological or hybridisation assays,
                                                                                                                                                                                                          A. victor
A. victor
                                                                       Engineere
Engineere
                                                                                                                                                                                                                                      Aaw76371 A. victor
Aab73552 Wild-type
Aae16038 Aequorea
Abg32365 Aequorea
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                                                                                                                                                                                            Aequorea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein; engineered fluorescent protein; reporter molecule; immunological assay; protein-protein interaction; fluorescence resonance energy transfer system; FRET system.
                                                                                                                     Aaw52321 | Aaw52319 | Aaw52318 |
                                                                                                                                                               Aaw52320 I
Aaw05304 C
Aaw24232 I
Aaw76105 I
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Aaw52329
Aaw52322
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AAW52329
AAW52322
AAW52321
AAW52319
                                                                                                                                                               AAW52320
AAW05304
AAW24232
                                                                                                                                                                                                          AAW76105
AAW40479
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AAB73552
AAE16038
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                                                                                                                                                                                                                                                                                     ABG32365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aequorea green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                         AAW52313 standard; protein; 238 AA
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96US-00706408.
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N-PSDB; AAV19946
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              version 5.1.6
- 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long
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0; Mismatches 0;
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/note= "Ser to Thr mutation"
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(UYOR-) UNIV OREGON.
(AURO-) AURORA BIOSCIENCES.
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Best Local Similarity
Matches 238; Conserv
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Nucleic acid encoding mutant green fluorescent proteins having longer

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This sequence is an engineered Aequorea victoria green fluorescent protein (GPP) of the invention, created from the sequence shown in AAM52313. The GPP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GPP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GPP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRETE (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and cutrher for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, constructions allow simultaneous measurements of at least 2 proteins when the constructions allows simultaneous measurements of at least 2 proteins when the constructions allow simultaneous measurements of the least 2 proteins in a cell. They are allow simultaneous measurements of at least 2 proteins when the constructions in a cell. They are allow simultaneous measurements of at least 2 proteins and cell. They are allow simultaneous measurements of at least 2 proteins and cell. They are allowed the constructions and cell. They are allowed the
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Pred. No. 1.3e-122;
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Misc-difference 65
/label= 865A
/note= "Ser to Ala mutation"
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                                                                                                               Claim 5; Page; 120pp; English.
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Best Local Similarity
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Aequorea victoria.
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fluorescence resonance energy transfer system; FRET system.

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This sequence is an engineered Aequorea victoria green fluorescent protein (GPP) of the invention, created from the sequence shown in protein (GPP) of the invention, created from the sequence shown in protein (GPP) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GPP) but differing by at least the substitution 7203x (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simulaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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97WO-US014593.
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96US-0070640B.
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Pred. No. 1.3e-122;
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                                                                    AAW52333 standard; protein; 238 AA
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                                                                                                   AAW52333;
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reporter molecule; immunological assay; protein-protein interaction;

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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW$2313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRBT (fluorescence resonance energy transfer) systems, e.g. for detecting protein interactions.

Cleavage of substrates and changes in potential across a membrane, and truther for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They cent, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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99.6%; Pred. No. 1.7e-122;
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Best Local Similarity 99.6%;
Matches 237; Conservative
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Aequorea victoria.
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Misc-difference
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30-AUG-1996;
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1 MSKGBELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL 60

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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW52313. The GFP DNA was mutated to produce the mucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having protein immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from Known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where photocoxicity and auto-fluorescence are reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding mutant green fluorescent proteins having longer wavelength emission - used as markers for probes and as components of fluorescent resonant energy transfer systems, also related vectors and
                                                                                                                                                                Green fluorescent protein; engineered fluorescent protein; reporter molecule; immunological assay; protein-protein interaction; fluorescence resonance energy transfer system; FRET system.
                                                                                                                                                                                                                                                                                                                                         /label= Gly, Thr, Ala, Leu, Cys, Val, Ile
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                                                                                                                              Engineered green fluorescent protein
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
               AAW52315 standard; protein; 238 AA.
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96US-00706408.
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                                                                                         (first entry)
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                                                                                                                                                                                                                                              Synthetic.
Aeguorea victoria.
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30-AUG-1996;
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AAW52315
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MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL 60

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Query Match 99.7%; Score 1266; DB 2; Length 238; Best Local Similarity 99.6%; Pred. No. 1.7e-122; Matches 237; Conservative 0; Mismatches 1; Indels 0

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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAM52313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resenance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are
                    NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                    NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
VTTPSYGVQCFSRYPDHMKRHDFPKSAMPEGYVQQRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                    YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                                                      Engineered green fluorescent protein.
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96US-0070640B.
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            allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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easily distinguished from known green and blue fluorescent proteins, so
                                                                                                                                                                                                                                                                                                                      YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding mutant green fluorescent proteins having longer wavelength emission - used as markers for probes and as components of fluorescent resonant energy transfer systems, also related vectors and
                                                                                                                                                                    VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRT1FFKDDGNYKTRAEVKFEGDTLV
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                                                                                            99.6%; Score 1265; DB 2;
99.6%; Pred. No. 2.1e-122;
ive 0; Mismatches 1;
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96US-00706408.
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                                                                                                                        Matches 237; Conservative
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                                                                                                           Similarity
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                                                                   Sequence 238 AA;
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30-AUG-1996;
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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW$2313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203x (x = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They cent, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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/label= His, Asn, Gln, Thr, Phe, Trp, Tyr
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99.6%; Pred. No. 2.1e-122;
ive 0; Mismatches 1;
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Matches 237; Conservative
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30-AUG-1996;
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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW52313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of RRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are assily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They cent, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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Pred. No. 2.1e-122;
/label= Y66W
/note= "Tyr to Trp mutation"
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Best Local Similarity 99.6
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cubitt AB,
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                                                                                   WO9806737-A1
                                                                                                                                                                                            15-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                             This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in protein (GFP) of the invention, created from the sequence shown in invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203x (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, transfer substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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                                                             Remington JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1265; DB 2;
Pred. No. 2.1e-122;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engineered green fluorescent protein Y66W.
                                                       Ormo MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers Misc-difference 66
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                                                                                                                                                                                                                                                                                                   Claim 47; Page; 120pp; English.
                                                          Heim R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.6%;
     (AURO-) AURORA BIOSCIENCES.
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                                                          Tsien RY, Cubitt AB,
                                                                                                               WPI; 1998-159454/14.
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Length 238; 0; Indels 9 9 120

Synthetic.

AAW52334;

(first entry)

10-JUL-1998

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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW32313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (II) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein interactions, cleavage of substrates and changes in potential across a membrane, and simultaneous measurements of at least 2 proteins in a cell. They entit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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                                                                                                                                                                   Green fluorescent protein; engineered fluorescent protein; reporter molecule; immunological assay; protein-protein interaction; fluorescence resonance energy transfer system; FRET system.
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0; Mismatches 1;
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                                                                                                Engineered green fluorescent protein.
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(AURO-) AURORA BIOSCIENCES.
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Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Aequorea victoria.
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30-AUG-1996;
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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAMS2313. The GFP DNA was mutated to produce the nucleic acids (I) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as components of FRET (fluorescent protein as expected monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy cransfer) systems, e.g. for detecting protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They cand auto-fluorescence are reduced.
121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                    YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                     181 YYQQYTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                    Green fluorescent protein; engineered fluorescent protein; reporter molecule; immunological assay; protein-protein interaction; fluorescence resonance energy transfer system; FRET system.
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                                                                                                                                                                                                                                                                                        Engineered green fluorescent protein S65C.
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(AURO-) AURORA BIOSCIENCES.
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                                                                                                                                                                                                                                                                                                                                                                                                              Aequorea victoria.
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Sequence 238 AA;

9

Gaps

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Gaps

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Length 238; Indels

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and having fluorescent properties different from GPP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, clavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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Pred. No. 2.1e-122;
0; Mismatches 1;
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96US-00706408.
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Best Local Similarity 99.6%;
Matches 237; Conservative (
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                                                                                                                                                                                                                                                                         Sequence 238 AA;
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/label= Ala, Val, Phe, Ser, Asp, Asn, Gln, Tyr, His, Cys
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fluorescence resonance energy transfer system; FRET system.
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                               Score 1265; DB 2;
Pred. No. 2.1e-122;
0; Mismatches 1;
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This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in the protein (GFP) of the invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent proteins (GFP) but differing by at least the substitution T203 (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for conjucting proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein interactions, cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They
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Nucleic acid encoding mutant green fluorescent proteins having longer wavelength emission - used as markers for probes and as components of fluorescent resonant energy transfer systems, also related vectors and
                                                                                                                                          Claim 47; Page; 120pp; English
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99.6%; Score 1265; DB 2; 99.6%; Pred. No. 2.1e-122; iive 0; Mismatches 1;
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Engineered green fluorescent protein. AAW52346 standard; protein; 238 AA 10-JUL-1998 (first entry) AAW52346; AAW52346

Green fluorescent protein; engineered fluorescent protein; mutein;

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reporter molecule, immunological assay, protein-protein interaction, fluorescence resonance energy transfer system; FRET system.

Synthetic. Aequorea victoria.

Location/Qualifiers /label= Phe, Tyr, Misc-difference 167

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19-FEB-1998

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invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequores green fluorescent proteins (II) having largely the same sequence as Aequores green fluorescent protein (GFP) but differing by at least the substitution T203X (X = H, Y, W or F) and having fluorescent properties different from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription.

They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting inotenin-protein interactions.

Cleavage of substrates and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They emit, and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
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99.6%; Pred. No. 2.1e-122;
ive 0; Mismatches 1;
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Matches 237; Conservative
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(UYOR-) UNIV
  L5-AUG-1997;
                                        16-AUG-1996;
30-AUG-1996;
                                                                                                                                                                                          Tsien RY,
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> AAW52324 standard; protein; 238 AA (first entry) 10-JUL-1998 AAW52324; AAW52324 **XXXXXXXXXX**

Green fluorescent protein; engineered fluorescent protein; mutein; reporter molecule; immunological assay; protein-protein interaction; Engineered green fluorescent protein Y66H.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention, which encode functional, engineered fluorescent proteins (II) having largely the same sequence as Aequorea green fluorescent protein (GFP) but differing by at least the substitution T203X (X.= H, Y, W or F) and having fluorescent protein from GFP. (II) are useful as reporter molecules in immunological or hybridisation assays, for monitoring proteins in cells and detecting induction of transcription. They are also useful as components of FRET (fluorescence resonance energy transfer) systems, e.g. for detecting protein-protein interactions, transfer) systems and changes in potential across a membrane, and further for making fluorescent substrates for protein kinase. (II) are easily distinguished from known green and blue fluorescent proteins, so allow simultaneous measurements of at least 2 proteins in a cell. They and are excited, at relatively long wavelengths where phototoxicity and auto-fluorescence are reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is an engineered Aequorea victoria green fluorescent protein (GFP) of the invention, created from the sequence shown in AAW52313. The GFP DNA was mutated to produce the nucleic acids (1) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIJFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VITFSHGVQCFSRYPDHMKRHDFFKSAMPEGYVQQRIIFFKDDGNYKTRAEVKFEGDILV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 YYQQNTPILDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding mutant green fluorescent proteins having longer wavelength emission - used as markers for probes and as components of fluorescent resonant energy transfer systems, also related vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEELFTAVVPILVELDGDVNGHKFSVSGEGEGDVTYGKLTLKFICTTGKLPVPWPTL
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Pred. No. 2.1e-122;
1; Mismatches 0; Indels 0
fluorescence resonance energy transfer system; FRET system.
                                                                                                                                                                                                                                                                                                                                                                                                                      Remington JS;
                                                                                                                        /label= Y66H
/note= "Tyr to His mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                    Ormo MF,
                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page; 120pp; English.
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(UYOR-) UNIV OREGON.
(AURO-) AURORA BIOSCIENCES.
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Matches 237; Conservative
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                                 Synthetic.
Aeguorea victoria
                                                                                                       Misc-difference
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30-AUG-1996;
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